



SEQUENCE LISTING

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<120> SOLUBLE CTLA4 MUTANT MOLECULES AND USES THEREOF

<130> 30436.30USI2

<140> 09/609,915

<141> 2000-07-03

<150> 07/723,617

<151> 1991-06-27

<150> 08/008,898

<151> 1993-01-22

<150> 08/228,208

<151> 1994-04-15

<150> 08/539,436

<151> 1995-10-05

<150> 09/014,761

<151> 1998-01-28

<150> 09/603,825

<151> 2000-06-26

<150> 60/036,594

<151> 1997-01-31

<160> 50

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Homo sapiens

<400> 1

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agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120

ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180

acagtgcttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240

gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300

gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
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 attgatccag aaccgtgccc agattctgac ttctctctct ggatccttgc agcagttagt 480
 tcgggggttgt ttttttatag ctttctcctc acagctgttt ctttgagcaa aatgctaaag 540
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<210> 2
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

a31
 cmf

Pro Cys Pro Asp Ser Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser
145 150 155 160

Ser Gly Leu Phe Phe Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser
165 170 175

Lys Met Leu Lys Lys Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys
180 185 190

Met Pro Pro Thr Glu Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe
195 200 205

Ile Pro Ile Asn
210

<210> 3
<211> 223
<212> PRT
<213> Homo sapiens

<400> 3

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1 5 10 15

Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20 25 30

Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45

Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60

Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80

Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr
85 90 95

Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 4
<211> 223
<212> PRT
<213> Mus musculus

<400> 4

Met Ala Cys Leu Gly Leu Arg Arg Tyr Lys Ala Gln Leu Gln Leu Pro
1 5 10 15

Ser Arg Thr Trp Pro Phe Val Ala Leu Leu Thr Leu Leu Phe Ile Pro
20 25 30

Val Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val Tyr Leu Ala
35 40 45

Ser Ser His Gly Tyr Ala Ser Phe Pro Cys Glu Tyr Ser Pro Ser His
50 55 60

Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr Asn Asp Gln
65 70 75 80

Met Thr Glu Val Cys Ala Thr Thr Phe Thr Glu Lys Asn Thr Val Gly
85 90 95

Phe Leu Asp Tyr Pro Phe Cys Ser Gly Thr Phe Asn Glu Ser Arg Val
 100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Leu
 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val Gly Met Gly
 130 135 140

Asn Gly Thr Gln Ile Tyr Tyr Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Tyr Ala Val Ser Leu Gly Leu Phe Phe
 165 170 175

Tyr Ser Phe Leu Val Ser Ala Val Ser Leu Ser Lys Met Leu Lys Lys
 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 210 215 220

<210> 5
 <211> 218
 <212> PRT
 <213> Mus musculus

<400> 5

Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
 1 5 10 15

Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Tyr Val
 20 25 30

Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
 35 40 45

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
 50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
 65 70 75 80

Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
85 90 95

Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
100 105 110

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
130 135 140

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Tyr Val Val Ala Gly Val
145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Tyr Met Asn Met
180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
210 215

<210> 6
<211> 218
<212> PRT
<213> Rattus norvegicus

<400> 6

Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Ser Phe Phe Ser Val Gln
1 5 10 15

Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Tyr
20 25 30

Asp Asn Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
35 40 45

31
cont.

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
65 70 75 80

Pro Asn Val Gly Phe Asn Cys Asp Gly Asn Phe Asp Asn Glu Thr Val
85 90 95

Thr Phe Arg Leu Trp Asn Leu Asp Val Asn His Thr Asp Ile Tyr Phe
100 105 110

Cys Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Ala
130 135 140

Gln Thr Ser Pro Lys Leu Phe Trp Pro Leu Val Val Val Ala Gly Val
145 150 155 160

Leu Leu Cys Tyr Gly Leu Leu Tyr Thr Val Thr Leu Cys Ile Ile Trp
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Ser Asp Tyr Met Asn Met
180 185 190

Thr Pro Arg Arg Leu Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
210 215

<210> 7
<211> 220
<212> PRT
<213> Homo sapiens

<400> 7

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1 5 10 15

Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30

Asp Asn Ala Tyr Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
 35 40 45

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
 50 55 60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
 65 70 75 80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
 85 90 95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
 100 105 110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
 115 120 125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 130 135 140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
 145 150 155 160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Tyr Thr Val Ala Phe Ile Ile
 165 170 175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 195 200 205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 210 215 220

<210> 8
 <211> 221
 <212> PRT
 <213> Gallus gallus

<400> 8

Met Leu Gly Ile Leu Val Val Leu Cys Leu Ile Pro Ala Ala Asp Val
1 5 10 15

Thr Glu Asn Lys Ile Leu Val Ala Gln Arg Pro Leu Leu Ile Val Ala
20 25 30

Asn Arg Thr Ala Thr Leu Val Cys Asn Tyr Thr Tyr Asn Gly Thr Gly
35 40 45

Lys Glu Phe Arg Ala Ser Leu His Lys Gly Thr Asp Ser Ala Val Glu
50 55 60

Val Cys Phe Ile Ser Trp Asn Met Thr Lys Ile Asn Ser Asn Ser Asn
65 70 75 80

Lys Glu Phe Asn Cys Arg Gly Ile His Asp Lys Asp Lys Val Ile Phe
85 90 95

Asn Leu Trp Asn Met Ser Ala Ser Gln Thr Asp Ile Tyr Phe Cys Lys
100 105 110

Ile Glu Ala Met Tyr Pro Pro Pro Tyr Val Tyr Asn Glu Lys Ser Asn
115 120 125

Gly Thr Val Ile His Tyr Arg Glu Thr Pro Ile Gln Thr Gln Glu Pro
130 135 140

Glu Ser Ala Thr Ser Tyr Trp Val Met Tyr Ala Val Thr Gly Leu Leu
145 150 155 160

Gly Phe Tyr Ser Met Leu Ile Thr Ala Val Phe Ile Ile Tyr Arg Gln
165 170 175

Lys Ser Lys Arg Asn Arg Tyr Arg Gln Ser Asp Tyr Met Asn Met Thr
180 185 190

Pro Arg His Pro Pro His Gln Lys Asn Lys Gly Tyr Pro Ser Tyr Ala
195 200 205

Pro Thr Arg Asp Tyr Thr Ala Tyr Arg Ser Trp Gln Pro
210 215 220

<210> 9

<211> 1152
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig

<400> 9
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agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
acagtgcttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacctg ggcataggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctgggtggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtgggtg 600
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg ggtgggtcagc 720
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc 780
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ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg cgtgggagtg ggagagcaat 960
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
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ccgggtaaat ga 1152

<210> 10
<211> 383
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig

<400> 10

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

<210> 11
<211> 1152
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: L104EIg

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agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
acagtgcttc ggcaggctga cagccaggtg actgaagtct gtgcggcaac ctacatgatg 240

gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
 gagctcatgt acccaccgcc atactacgag ggcataggca acggaacca gatttatgta 420
 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
 acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 540
 ccaaaacca aggacacct catgatctcc cggacccttg aggtcacatg cgtggtggtg 600
 gacgtgagcc acgaagaccc tgagggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc 780
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
 gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccacg cctcccgatg tggactccga cggctccttc 1020
 ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
 tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
 ccgggtaaat ga 1152

<210> 12
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: L104EIg

<400> 12

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg

50

55

60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

<210> 13
<211> 1152
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: L104EA29YIg

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agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180
acagtgcttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggt acgtggacgg cgtggagggtg 660

a37
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cataatgccca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720
 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc 780
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
 gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
 ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
 tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
 ccgggtaaat ga 1152

<210> 14
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: L104EA29YIg

<400> 14

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

a37
 cont

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg

a37
 Cont.

340

345

350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

<210> 15
 <211> 1152
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: L104EA29LIg

<400> 15

atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgact cctgtttcca 60
 agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
 ggcacgcta gctttgtgtg tgagtatgca tctccaggca aattgactga ggtccgggtg 180
 acagtgcttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
 gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
 gagctcatgt acccaccgcc atactacgag ggcataggca acggaacca gatttatgta 420
 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
 ccaaaacca aggacacct catgatctcc cggaccctg aggtcacatg cgtgggtggtg 600
 gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
 gtctcaccg tctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
 gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
 ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
 ttctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
 tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140

a37
amt.

ccgggtaaat ga

1152

<210> 16

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: L104EA29LIg

<400> 16

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

Tyr Ala Ser Pro Gly Lys Leu Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
 260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

<210> 17

<211> 1152

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: L104EA29TIg

<400> 17

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agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aaactactga ggtccgggtg 180
acagtgcttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacgag ggcataggca acggaacca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 540
ccaaaacca aggacacctt catgatctcc cggaccctg aggtcacatg cgtggtggtg 600
gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc 780
aaciaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
ccgggtaaat ga 1152

<210> 18

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: L104EA29TIg

<400> 18

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala

1	5	10	15
Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro	20	25	30
Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu	35	40	45
Tyr Ala Ser Pro Gly Lys Thr Thr Glu Val Arg Val Thr Val Leu Arg	50	55	60
Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met	65	70	75
Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser	85	90	95
Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp	100	105	110
Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr	115	120	125
Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu	130	135	140
Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His	145	150	155
Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val	165	170	175
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr	180	185	190
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu	195	200	205
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys	210	215	220
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser	225	230	235
			240

a37
cont.

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

<210> 19
<211> 1152
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: L104EA29WIg

<400> 19
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agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatggactga ggtccgggtg 180
acagtgcttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300

gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
 acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 540
 ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 600
 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 660
 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720
 gtcctcaccg tcttgacca ggactgggtg aatggcaagg agtacaagtg caaggtctcc 780
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccagc cctcccgtgc tggactccga cggctccttc 1020
 ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
 tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
 ccgggtaaat ga 1152

<210> 20
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: L104EA29WIg

<400> 20

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

Tyr Ala Ser Pro Gly Lys Trp Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

a37
 cont.

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

237
cont.

290

295

300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375 380

<210> 21
 <211> 65
 <212> DNA
 <213> Homo sapiens

<400> 21
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 cagcc 65

<210> 22
 <211> 33
 <212> DNA
 <213> Homo sapiens

<400> 22
 tttgggctcc tgatcagaat ctgggcacgg ttg 33

<210> 23
 <211> 72
 <212> DNA
 <213> Homo sapiens

<400> 23
 ctagccactg aagcttcacc aatgggtgta ctgctcacac agaggacgct gctcagtctg 60
 gtccttgac tc 72

<210> 24
 <211> 33
 <212> DNA

<213> Homo sapiens

<400> 24

gcaatgcacg tggcccagcc tgctgtggta gtg

33

<210> 25

<211> 45

<212> DNA

<213> Homo sapiens

<400> 25

tgatgtaaca tgtctagatc aattgatggg aataaaataa ggctg

45

<210> 26

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oncostatin M signal peptide forward primer

<400> 26

ctagccactg aagcttcacc atgggtgtac tgctcacac

39

<210> 27

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oncostatin M signal peptide reverse primer

<400> 27

tggcatgggc tcctgatcag gcttagaagg tccgggaaa

39

<210> 28

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oncostatin M signal peptide reverse primer

<400> 28

tttgggctcc tgatcaggaa aatgctcttg cttggttgt

39

<210> 29

<211> 84

<212> DNA

a37
ant

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human IgCgamma1 forward primer

<400> 29

aagcaagagc attttcctga tcaggagccc aaatcttctg acaaaactca cacatcccca 60

ccgtccccag cacctgaact cctg 84

<210> 30

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human IgCgamma1 reverse primer

<400> 30

cttcgaccag tctagaagca tcctcgtgcg accgcgagag c 41

<210> 31

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CD5Ig forward primer

<400> 31

cattgcacag tcaagcttcc atgcccattg gttctctggc caccttg 47

<210> 32

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CD5Ig reverse primer

<400> 32

atccacagtg cagtgatcat ttggatcctg gcatgtgac 39

<210> 33

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDM8 forward primer

a37
cont

<400> 33
aatacgactc actatagg 18

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDM8 reverse primer

<400> 34
caccacactg tattaacc 18

<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4/CD28

<400> 35

Met Tyr Pro Pro Pro Tyr
1 5

<210> 36
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig mutant fusion protein

<400> 36

Ala Tyr Pro Pro Pro Tyr
1 5

<210> 37
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig mutant fusion protein

<400> 37

Met Ala Pro Pro Pro Tyr
1 5

a37
cont.

<210> 38
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig mutant fusion protein
<400> 38

Met Tyr Ala Pro Pro Tyr
1 5

<210> 39
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig mutant fusion protein
<400> 39

Met Tyr Pro Ala Pro Tyr
1 5

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4/CD28Ig mutant fusion protein
<400> 40

Met Tyr Pro Pro Ala Tyr
1 5

<210> 41
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4/CD28Ig mutant fusion protein
<400> 41

Met Tyr Pro Pro Pro Ala
1 5

a37
Cont

<210> 42
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4Ig mutant fusion protein

<400> 42

Ala Ala Pro Pro Pro Tyr
1 5

<210> 43
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> k is either c, g or t

<220>
<221> misc_feature
<222> (28)..(29)
<223> n is either a, c, g or t

<220>
<221> misc_feature
<222> (30)..(30)
<223> k is either c, g or t

<220>
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<220>
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<222> (33)..(33)
<223> k is either c, g or t

<220>
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<223> n is either a, c, g or t

<220>
<221> misc_feature
<222> (36)..(36)

a37
Cont

<223> k is either c, g or t

<220>

<221> misc_feature

<222> (37)..(38)

<223> n is either a, c, g or t

<220>

<221> misc_feature

<222> (39)..(39)

<223> k is either c, g or t

<220>

<221> misc_feature

<222> (40)..(41)

<223> n is either a, c, g or t

<220>

<221> misc_feature

<222> (42)..(42)

<223> k is either c, g or t

<220>

<221> misc_feature

<222> (43)..(44)

<223> n is either a, c, g or t

<220>

<221> misc_feature

<222> (45)..(45)

<223> k is either c, g or t

<220>

<221> misc_feature

<222> (46)..(47)

<223> n is either a, c, g or t

<220>

<221> misc_feature

<222> (48)..(48)

<223> k is either c, g or t

<220>

<221> misc_feature

<222> (49)..(50)

<223> n is either a, c, g or t

A37
Cont.

<220>
 <221> misc_feature
 <222> (51)..(51)
 <223> k is either c, g or t

<400> 43
 cgaggcatcg ctagctttgt gtgtgagnnk nnknnknnkn nknnknnknn kgagggtccgg 60
 gtgacagt 68

<210> 44
 <211> 59
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Phage display reverse primer

<400> 44
 gggtgccgca cagacttcgg tcacctggct gtcagcctgc cgaagcactg tcacccgga 59

<210> 45
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CTLA4 mutant

<400> 45

Phe Glu Pro Lys Arg Gly Val Gln
 1 5

<210> 46
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: CTLA4 mutant

<400> 46

Trp Asp Gln Tyr Thr Gly Tyr Gly
 1 5

<210> 47
 <211> 8
 <212> PRT
 <213> Artificial Sequence

a37
 Cont

<220>
<223> Description of Artificial Sequence: CTLA4 mutant

<400> 47

Trp Asp Ala Tyr Arg Asn Gln Gln
1 5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4 mutant

<400> 48

Tyr Asp His Pro Tyr Asp Gly Gln
1 5

<210> 49
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4 mutant

<400> 49

Trp Asp Gln His Val Ser Arg Arg
1 5

37
a
cont
<210> 50
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CTLA4

<400> 50

Tyr Ala Ser Pro Gly Lys Ala Thr
1 5